

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 24, 1999, 00:40:12 ; Search time 366.45 Seconds  
(without alignments)  
87.864 Million cell updates/sec

Title: US-09-205-015-1  
Perfect score: 9  
Sequence: 1 tctgagtca 9

Scoring table: IDENTITY\_NUC

Searched: 808301 seqs, 1788773984 residues

Database : GenEmbl.\*

- 1: gb\_bal.\*
- 2: gb\_ba2.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl1.\*
- 9: gb\_pl2.\*
- 10: gb\_pr1.\*
- 11: gb\_pr2.\*
- 12: gb\_pr3.\*
- 13: gb\_ro.\*
- 14: gb\_st.\*
- 15: gb\_sy.\*
- 16: gb\_un.\*
- 17: gb\_vl.\*
- 18: gb\_htg.\*
- 19: em\_ba.\*
- 20: em\_fun.\*
- 21: em\_hum1.\*
- 22: em\_hum2.\*
- 23: em\_in.\*
- 24: em\_om.\*
- 25: em\_or.\*
- 26: em\_ov.\*
- 27: em\_pat.\*
- 28: em\_ph.\*
- 29: em\_pl.\*
- 30: em\_ro.\*
- 31: em\_sy.\*
- 32: em\_un.\*
- 33: em\_vl.\*
- 34: em\_htg.\*
- 35: em\_sts.\*
- 36: gb\_bal.\*
- 37: gb\_ba2.\*
- 38: gb\_pl1.\*
- 39: gb\_pl2.\*
- 40: gb\_pr1.\*
- 41: gb\_pr2.\*
- 42: gb\_pr3.\*
- 43: gb\_sts.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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C	1	9	100.0	148068	1	AB001488
C	2	9	100.0	24907	1	AB002668
C	3	9	100.0	24907	1	AB002668
C	4	9	100.0	1907	1	AB003186
C	5	9	100.0	1933	1	AB008139
C	6	9	100.0	1950	1	AB008153
C	7	9	100.0	15295	1	AB010150
C	8	9	100.0	2748	1	ACCP5X
C	9	9	100.0	2878	1	ACMP5EH
C	10	9	100.0	14801	1	AE000688
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C	13	9	100.0	15467	1	AE000723
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C	21	9	100.0	9938	1	AE000870
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ALIGNMENTS

RESULT 1  
AB001488/c  
LOCUS  
DEFINITION  
ACCESSION  
NID  
KEYWORDS

AB001488 148068 bp DNA  
Bacillus subtilis genome sequence, 148 kb sequence of the region  
between 35 and 47 degree.  
g1881226

21-OCT-1997

BCT

alr: cspC; ddaA; dinB; exp2; gslB; mutT; nap; orfR; orfS; orfT;  
rsbU; rsbV; rsbW; sigB; sigE; ydaA; ydaB; ydaC; ydaD; ydaE;  
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ydgA; ydgB; ydgC; ydgD; ydgE; ydgF; ydgG; ydgH; ydgI; ydgJ; ydgK;  
Bacillus subtilis (strain:168) DNA.

SOURCE  
ORGANISM

REFERENCE	Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Bacillaceae; _Bacillus.
AUTHORS	Beloin,C., Ayora,S., Exley,R., Hirschbein,L., Ogasawara,N., Kasahara,Y., Alonso,J.C. and Hegarat,F.L.
TITLE	Characterization of an lrp-like (lrpC) gene from Bacillus subtilis
JOURNAL	Mol. Gen. Genet. 256 (1), 63-71 (1997)
MEDLINE	98000887
REFERENCE	2 (sites)
AUTHORS	Kasahara,Y., Nakai,S., Lee,S., Sadale,Y. and Ogasawara,N.
TITLE	A 148 kbp sequence of the region between 35 and 47 degree of the Bacillus subtilis genome
JOURNAL	Unpublished (1997)
AUTHORS	3 (bases 1 to 148068)
TITLE	Ogasawara,N.
JOURNAL	Direct Submission
AUTHORS	Submitted (03-MAR-1997) to the DBJ/EMBL/GenBank databases. Naotake Ogasawara, Nara Institute of Science and Technology, Graduate School of Biological Sciences; 8916-5 Takayama-cho, Ikoma, Nara 630-01, Japan (E-mail:nogasawa@bs.ais-t-nara.ac.jp, Tel:07437-2-5430, Fax:07437-2-5439)
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terminator

gene

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CDS

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RBS

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CDS

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terminator

gene

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gene

RBS

CDS

gene

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53656..54070
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53656..53660
/gene="orfM"
53669..54070
/gene="orfM"
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/db_xref="PID:g1881279"
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54089..55089
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54089..54075
/gene="rsbU"
54082..55089
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/codon_start=1
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/db_xref="PID:g1881280"
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PAALCMSIKYAMDSPETGHPHQVILKNLRVVEQNVDSMFTIMFYANMDKHQF
TYASAGHPGPGFYQKONTFYDLEAKGLVIGISQDYDKQFDQHLKRGDMIVLFSQGV
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V"
55139..55480
/gene="rsbV"
55139..55145
/gene="rsbV"
55151..55480
/gene="rsbV"
/feature="SIMILAR PRODUCT IN SYNECHOCYSTIS."
/codon_start=1
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/db_xref="PID:d1020061"
/db_xref="PID:g1881281"
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RICLDKSVISMDSTGLGVFGTFKMKVKKGGSKLENLSERLIRLFDITGLKDIIDISA
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55462..55959
/gene="rsbW"
55462..55469
/gene="rsbW"

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CDS      55477..55959
/gene="rsb"
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RBSW)"
/db_xref="PID:d1020062"
/db_xref="PID:g1881282"
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gene      55909..56713
/gene="sigB"
RBS      55909..55914
/gene="sigB"
CDS      55919..56713
/gene="sigB"
/codon_start=1
/transl_table=11
/product="RNA POLYMERASE SIGMA-B FACTOR (SIGMA-37)"
/db_xref="PID:d1020063"
/db_xref="PID:g1881283"
/transl_table="MIMTOPSKTKTKDEVDRLISDYOTKODEQAQETLVRYTNLV
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YQALSDHSTEADSDGSTVILDIVGSDQEDGYERNQQLMSLVHLSDBREKQIIDL
TYIONKSQKETGDLGILGISQMHVSRLQKAVKRLREALIEDPSNMLM"
RBS      56699..56705
/gene="rsbX"
gene      56699..57312
/gene="rsbX"
CDS      56713..57312
/gene="rsbX"
/codon_start=1
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REGION)"
/db_xref="PID:d1020064"
/db_xref="PID:g1881284"
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PDIRSLHKGQSVVEEISLSLKMYSRKDDLLIYLGOLS"
terminator 57321..57353
/note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
gene      57539..57848
/gene="ydcF"
RBS      57539..57544
/gene="ydcF"
CDS      57555..57848
/gene="ydcF"
/note="FUNCTION UNKNOWN."
/codon_start=1
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RBS      57833..57840
/gene="ydcG"
gene      57833..58285
/gene="ydcG"
CDS      57845..58285
/gene="ydcG"
/note="FUNCTION UNKNOWN, SIMILAR PRODUCT IN BACILLUS
LICHENIFORMIS."
/codon_start=1
/transl_table=11
/db_xref="PID:d1020066"
/db_xref="PID:g1881286"
/transl_table="MNTNYIGWVSEQHVLYKGAAGGFAQLCHGKKAPLAKMKEGDWLI
terminator 61137..61165
/note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
gene      61351..61817
/gene="ydcK"
RBS      61351..61360
/gene="ydcK"
CDS      61365..61817
/gene="ydcK"
/note="FUNCTION UNKNOWN."
/codon_start=1
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/db_xref="PID:d1020070"
/db_xref="PID:g1881290"
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NIELNRKYLIEHGRELIGILIKHELCHYHLHLEKGYKHDRDFMLLQOVNAPRECT
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61940..62014
/product="trna-Asn"

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YSPRDAYPDGKLLRSFTAIGKVKSGNIYPYOMAPNEIPYRLDIDYVPCHKIGFYDIK
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58253..58260
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58253..58712
/gene="ydcH"
58269..58712
/gene="ydcH"
/note="FUNCTION UNKNOWN."
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58791..58795
/gene="ydcI"
58791..60818
/gene="ydcI"
58806..60818
/gene="ydcI"
/note="FUNCTION UNKNOWN, SIMILAR PRODUCT IN E. COLI, H.
INFLUENZAE AND NEISSERIA MENINGITIDIS."
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IEGAKHIIAQISDEPTFRKWIQETFRKGTIKSAAGKSADTDEKNVYEMVYEETI
AKVVPVHRVLAAMNREKEDILKVALEPADHIAKVLKQIINKBSTSVREILOETIEDS
YKRLIQAIREIRKELSEKADQAHIFSENARKLLQPPMKGVTLGVDPAPRTGC
KLAVSDETGKVLKIDVIYPHAPVNTKEAHEKVKKILEQYQVEMVAINGSTASRETEQ
FVNVLRDMPKKIYIIVNAGASVYSASELAREFPDLKVEERSAVSIARRLODPLA
ELVKIDPKSVGQYQHDVSKRLNESLREFTVTVNOGVNVNTASAAALQYVAGLS
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60750..60754
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60750..61138
/gene="ydcJ"
60767..61138
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VTVMVDGVQKGVSLSVK"
61137..61165
/note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
61351..61817
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61351..61360
/gene="ydcK"
61365..61817
/gene="ydcK"
/note="FUNCTION UNKNOWN."
/codon_start=1
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61940..62014
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69640..69906  
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IIVOTLAVINNAKLQATNILEDEMETDERSVEFEGSIYE"  
RBS      69905..69913  
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/gene="yddA"  
69923..70231  
/gene="yddA"  
/note="FUNCTION UNKNOWN."  
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RBS      70205..70210  
/gene="yddB"  
70205..71285  
/gene="yddB"  
70212..71285  
/gene="yddB"  
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TRANSPOSON TN916."  
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LYNKEDKNSLFQYKVTYENLYPVEKEVEKDGKKKVKVKNEKYEKQMLL  
NIPVTNKGDSFVAVPYFTQIYDLKGDIAFKGKETRDEYAGEKKESTESPL  
KYASKEKEVMYMKPEALEGNLFGVQSVKIPETKKGFEVFCVAFREKENDIP  
NEKFSLEITENSQFYVNLKHQ"  
RBS      71284..71290  
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71284..71545  
/gene="yddC"  
71297..71545  
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/note="FUNCTION UNKNOWN."  
/codon_start=1  
/transl_table=11  
/db_xref="PID:d1020082"  
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RBS      71544..71549  
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71544..72082  
/gene="yddD"  
71558..72082  
/gene="yddD"  
/note="FUNCTION UNKNOWN."  
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/db_xref="PID:d1020083"  
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GVLPNNKQFDSYAK"  
RBS      71951..71959  
/gene="yddE"  
71951..74465  
/gene="yddE"  
71970..74465  
/gene="yddE"  
/note="SIMILAR TO ORF16 OF ENTEROCOCCUS FAECALIS  
TRANSPOSON TN916."  
/codon_start=1  
/transl_table=11  
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FEKVEEVEETLANIMASVGRSELSETEVINRHFVRGLHQHQTNESEIKDVKSITN  
TIIDPTDPSVHLHSDQDEGSFAFVDEFLHNSSEDLFYEAQSLFFPVEVQMKIQ  
ESKSTIPALNKRQQLKEQEQSTGDRSDSVSTVSATMIRHLODEIKEDYHVMN  
WLSVIVVHGKTKECVGKATIVRHLKAGITCLPVLADQNLFLYKMLPGEKLDITDK  
NWIQTTQDGVASFLAVNSDIGSKIGFGLGWDFRQETDLSAIMSSRDFVLHFP  
LANQOLKSGKTRSPHCLITGDTGSKSYLAKLIFNYISMLNIKSLYIDPKKELWQ  
RVNDEKIRENPLYIAHLEKYNITLDHENTHNGALDISFLPMKAKELVOVIFE  
OYVDEKGDINTAFRLKATSEVIDAKONGQGVGLDIIRKMQSHPEEAVOKAGDYLNE  
VVSILKLCIHGDSNPALSLEKRITILEVENMDLPDHAERLENYITSLKSAVMAFA  
LGKFCELFGMNQDEQTEFFIDEAWIFTTSQKKVQMRRIGRISNAYYFISQSK  
DALKEEDSGNFVAFADPEPNEREREVLKMMMEYTKDKNKKMESMFQOCLEKDYGR  
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RBS      74466..74810  
/gene="yddF"  
74466..74476  
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74484..74810  
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/note="FUNCTION UNKNOWN."  
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LLTPLD"  
RBS      74809..74816  
/gene="yddG"  
74809..77261  
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74814..77261  
/gene="yddG"  
/note="FUNCTION UNKNOWN."  
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/db_xref="PID:g1881306"  
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CVVIGLWGNAGYKMYKLVNLASVEAQGLTAGLVIGVQDEGNFADSSAIEKKG  
EMEGTAVMENLYDIAMKLPFLIVNDETSEKINEEDTDGKLNRIDKLLSYKLSE  
DGEKDKDYIKETEIDDYKNESMTSGVNEOLGESITAVVASIVIGIPILAFNFI  
LOVVALVIVFVFAPFILAYPOLAYSGVTLGLRGLSVILLKAMGLVIVLVYTCFI  
VQKLIPENGSGMYLLAVLASILNIGFHKRDLIIFVITAGKVVSVDDNMENRQNI  
VQPAEQAKKIGVWNGGVFTFTNHFGRKDGSDAGVTGAPSGGNSPSGTAMG  
IDNTHAISRTPTKETANGIANHNSRLKRNPTLSKEQKQKQKAFANENKQOSH  
LARLRKDGINSPLKDALNEGDELSKRAPILQDKKDESKARTQKQYVQLLKQPNQ  
QOTDDASLQHEESTSNRAVLOENEDTERTDQKAYIYDEQNQLETQOQDFEQK  
DDSVSNSEPAQKETAIEKRSQKVMNQPEQLGESQSPQSKVQENQPIANERKLRP  
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RSSKVEDRLRDRTER"  
RBS      77240..77248  
/gene="yddH"  
77240..78247  
/gene="yddH"  
77258..78247  
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complement(106671..107254)
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complement(106671..107243)
/gene="yden"
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complement(107248..107254)
/gene="yden"
107894..108780
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107894..107901
/gene="ydeQ"
107908..108780
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LFLNLFVIFVSTVFGLOGLLSVIAYIASKVIHVVEEGLSGSKTFQIITTOPELMV
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INFLUENZAE AND SYNECHOCYSTIS."
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109413..110020
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109413..109421
/gene="ydeQ"
109427..110020
/gene="ydeQ"
/feature="PROBABLE NAD(P)H OXIDOREDUCTASE."
/codon_start=1
/transl_table=11
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/db_xref="PID:g1881337"
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EIASANRYKHITNIELNPKVRLQRLKQLESVDLT"
110110..110155
/feature="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
complement(110164..111367)

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/gene="ydeR"
complement(110164..111351)
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CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES
VENEZUELAE."
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VADIMWNAIFALSVAQSVILAVLSKVPARKPTANTYNTALLGSMWKLRTTPVLR
RRAIYAFVFGAFSLFTVTPLLLSGPDFHFSQKALALYALVGLAGVATAPIGGLAD
RGLRLATGIALGVVVSLLPLMIQSSSPVGIIVLVNAAAILLDMGVSANVLQSRAI
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TEK"
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RBS
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111539..112151
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111539..111549
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111555..112151
/gene="ydes"
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STREPTOMYCES HYGROSCOPICUS."
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112745..113094
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/gene="ydeR"
112759..113094
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ARSENICAL RESISTANCE OPERON REPRESSOR."
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113093..114414
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113093..113099
/gene="ydfa"
113107..114414
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terminator

gene

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Query Match 100.0%; Score 9; DB 1; Length 148068;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
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Db 119312 TCTGAGTCA 119304

RESULT 2
AB002668 24907 bp DNA BCT 21-FEB-1998
LOCUS Actinobacillus actinomycetemcomitans DNA for glycosyltransferase,
DEFINITION lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.
ACCESSION AB002668
NID g1944153
KEYWORDS rhamnosyltransferase; glycosyltransferase; exonuclease III;
galactosyltransferase; rhamnosyltransferase; ABC transport protein;
dTDP-4-keto-6-deoxy-D-glucose-3,5-epimerase; dTDP-4-rhamnose
reductase; glucose-1-phosphate-thymidyltransferase e;
dTDP-D-glucose-4,6-dehydratase; lytic transglycosylase.
SOURCE Actinobacillus actinomycetemcomitans (strain:Y4) DNA.
ORGANISM Actinobacillus actinomycetemcomitans
Eubacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
REFERENCE 1 (sites)
AUTHORS Yoshida,Y., Nakano,Y., Yamashita,Y. and Koga,T.
TITLE Identification of a genetic locus essential for serotype b-specific
antigen synthesis in Actinobacillus actinomycetemcomitans
JOURNAL Infect. Immun. 66 (1), 107-114 (1998)
MEDLINE 98084462
REFERENCE 2 (bases 1 to 24907)
AUTHORS Yoshida,Y.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1997) to the DBJ/EMBL/GenBank Databases. Yasuo
Yoshida, Kyushu University Faculty of Dentistry, Department of
Preventive Dentistry; 3-1-1 Maidashi, Higashi-Ku, Fukuoka, Fukuoka
812-82, Japan (E-mail: yasuo@haembox.nc.kyushu-u.ac.jp,
Tel:092-642-6423, Fax:092-642-6354)
FEATURES
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rhamnosyltransferase; glycosyltransferase; exonuclease III;  
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reductase; glucose-1-phosphate-thymidyltransferase e;  
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Actinobacillus actinomycetemcomitans  
Actinobacillus actinomycetemcomitans (strain:Y4) DNA.  
Eubacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
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1 (sites)  
Yoshida,Y., Nakano,Y., Yamashita,Y. and Koga,T.  
Identification of a genetic locus essential for serotype b-specific  
antigen synthesis in Actinobacillus actinomycetemcomitans  
Infect. Immun. 66 (1), 107-114 (1998)  
JOURNAL  
MEDLINE  
9808462  
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2 (bases 1 to 24907)  
Yoshida,Y.

TITLE  
JOURNAL  
FEATURES  
source

Direct Submission  
Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo  
Yoshida, Kyushu University Faculty of Dentistry, Department of  
Preventive Dentistry; 3-1-1 Maidashi, Higashi-ku, Fukuoka, Fukuoka  
812-82, Japan (E-mail: yasuo@box.nc.kyushu-u.ac.jp,  
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DEFINITION complete cds.  
ACCESSION AB003186  
NID 92055257  
KEYWORDS polyhydroxybutyrate depolymerase  
SOURCE Comamonas acidovorans (strain:YML1609) DNA.  
ORGANISM Comamonas acidovorans  
REFERENCE 1 (sites) Eubacteria; Proteobacteria; beta subdivision; Comamonas.  
AUTHORS Kasuya,K., Inoue,Y., Tanaka,T., Akehata,T., Iwata,T., Fukui,T. and  
DOI,Y.  
TITLE Biochemical and molecular characterization of the  
polyhydroxybutyrate depolymerase of Comamonas acidovorans YML1609,  
isolated from freshwater  
Appl. Environ. Microbiol. 63 (12), 4844-4852 (1997)  
JOURNAL 98069478  
MEDLINE 2 (bases 1 to 1907)  
REFERENCE Kasuya,K.  
AUTHORS Direct Submission  
TITLE Submitted (18-APR-1997) to the DBJ/EMBL/GenBank databases.  
JOURNAL Ken-ichi Kasuya, The Institute of Physical and Chemical Research  
(RIKEN), Polymer Chemistry Lab.; Hirosawa 2-1, Wako, Saitama  
351-01, Japan (E-mail:kkasuya@postman.riken.go.jp,  
Tel.048-462-1111, Fax:048-462-4667)  
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Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Qy      1 tctgagtcga 9
Db      1662 TCTGAGTCA 1654

RESULT' 5
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LOCUS   AB008139      1933 bp      DNA      BCT      21-MAR-1998
DEFINITION   Enterobacter gergoviae gene for GroES protein homologue, GroEL protein homologue, partial cds.
ACCESSION   AB008139
NID        92980903
KEYWORDS   GroES protein homology; GroEL protein homology.
SOURCE     Enterobacter gergoviae (strain:JCM 1234) DNA.
ORGANISM   Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Enterobacter.
REFERENCE   1 (sites)
AUTHORS     Harada,H. and Ishikawa,H.
TITLE       Phylogenetical relationship based on groE genes among phenotypically related Enterobacter, Pantoea, Klebsiella, Serratia, and Erwinia species
JOURNAL     J. Gen. Appl. Microbiol. 43, 355-361 (1997)
REFERENCE   2 (bases 1 to 1933)
AUTHORS     Harada,H.
TITLE       Direct Submission
JOURNAL     Submitted (15-OCT-1997) to the DBJ/EMBL/GenBank databases. Hosami Harada, Graduate School of Science, University of Tokyo, Department of Biological Sciences; Hongo, Bunkyo-ku, Tokyo 113, Japan, Bunkyo-ku, Tokyo 113, Japan (E-mail:hosami@biol.s.u-tokyo.ac.jp, Tel:03-3812-2111, Fax:03-3816-1965)
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1356 TCTGAGTCA 1348

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RESULT 6
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DEFINITION   Erwinia aphidicola gene for GroES protein homologue, GroEL protein homologue, partial cds.
ACCESSION   AB008153
NID        92980945
KEYWORDS   GroES protein homology; GroEL protein homology.
SOURCE     Erwinia aphidicola (strain:IAMI4479) DNA.
ORGANISM   Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Erwinia.
REFERENCE   1 (sites)
AUTHORS     Harada,H. and Ishikawa,H.
TITLE       Phylogenetical relationship based on groE genes among phenotypically related Enterobacter, Pantoea, Klebsiella, Serratia, and Erwinia species
JOURNAL     J. Gen. Appl. Microbiol. 43, 355-361 (1997)
REFERENCE   2 (bases 1 to 1950)
AUTHORS     Harada,H.
TITLE       Direct Submission
JOURNAL     Submitted (15-OCT-1997) to the DBJ/EMBL/GenBank databases. Hosami Harada, Graduate School of Science, University of Tokyo, Department of Biological Sciences; Hongo, Bunkyo-ku, Tokyo 113, Japan, Bunkyo-ku, Tokyo 113, Japan (E-mail:hosami@biol.s.u-tokyo.ac.jp, Tel:03-3812-2111, Fax:03-3816-1965)
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BASE COUNT      511 a      474 c      577 g      388 t
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1373 TCTGAGTCA 1365

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DEFINITION
ACCESSION      ABO10150
NID      93142207
KEYWORDS      mannose-6-phosphate dehydrogenase; ATP binding component of ABC-transporter;
              phosphomannomutase; GDP-mannose pyrophosphorylase;
              gluconate-6-phosphate dehydrogenase; integral membrane component of
              ABC-transporter
SOURCE      Escherichia coli (strain:F492) DNA, clone_lib:31 clone:PTS08.
ORGANISM      Escherichia coli
              Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
              Escherichia.
REFERENCE      1 (sites)
AUTHORS      Sugiyama,T., Kido,N., Kato,Y., Koide,N., Yoshida,T. and Yokochi,T.
TITLE      Generation of escherichia coli O9a serotype, a subtype of E. coli
              O9, by transfer of the wb* gene cluster of klebsiella O3 into E.
              coli via recombination
JOURNAL      J. Bacteriol. 180 (10), 2775-2778 (1998)
MEDLINE      98241545
REFERENCE      2 (sites)
AUTHORS      Sugiyama,T., Kido,N., Koide,N., Kato,Y., Yoshida,T., Jiang,G.,
              Paeng,N., Takahashi,K., Morikawa,A. and Yokochi,T.
TITLE      Nucleotide sequence of Escherichia coli O8 wb gene cluster
              unpublished (1998)
REFERENCE      3 (bases 1 to 15295)
AUTHORS      Sugiyama,T.
TITLE      Direct Submission
JOURNAL      Submitted (07-JAN-1998) to the DDBJ/EMBL/Genbank databases.
              Tsuyoshi Sugiyama, Aichi Medical University, Department of
              Microbiology and Immunology; Yazako, Nagakute, Aichi 480-11, Japan
              (E-mail:sugiyama@aichi-med-u.ac.jp, Tel:0561-62-3311,
              Fax:0561-63-9187)
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gene
CDS

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RBS
gene
CDS

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RBS
gene
CDS

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TIOLOGEVDDLSHVIDONHQLHQQMADLHNSRWITQPLEWLSIORQLLRQEGAKV  
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-10\_signal

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11579. .11582  
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BASE COUNT 3607 a 3701 c 4063 g 3924 t  
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Query Match 100.0%; Score 9; DB 1; Length 15295;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 tctgagtc a 9  
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Db 7480 TCTGAGTCA 7488  
RESULT 8  
ACCPSTM/c. 2748 bp DNA BCT 19-OCT-1994  
LOCUS A.calcoaceteticus epsx and epsm genes.  
DEFINITION X81320  
ACCESSION 9559387  
NID epsx; epsx; GDP-mannose pyrophosphorylase; phosphomannose  
isomerase.  
SOURCE Acinetobacter calcoaceteticus.  
ORGANISM Acinetobacter calcoaceteticus  
Eubacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  
Acinetobacter.  
REFERENCE 1 (bases 1 to 2748)  
AUTHORS Stark,M. and Kaplan,N.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2748)  
AUTHORS Stark,M.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-1994) M. Stark, Tel Aviv University, Dept of  
Molecular Microbiology & Biotechnology, Ramat-Aviv, 69978 Tel-Aviv,  
ISRAEL  
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WSALWDIQDKDDQGNVIQGDVITVKSQNNYVFSRSLVSLGLVDNVLVIETKDALIVA  
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Query Match 100.0%; Score 9; DB 1; Length 2748;

Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgagtcga 9  
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 Db 1793 TCTGAGTCA 1785

RESULT 9

ACIMPDEH ACIMPDEH 2878 bp DNA BCT 01-SEP-1992  
 LOCUS A.calcoaceticus gene for inosin-5-monophosphate dehydrogenase and a  
 DEFINITION putative ferredoxin.  
 ACCESSION X6859  
 NID 938718

KEYWORDS ferredoxin; inosine-5'-monophosphate dehydrogenase.  
 SOURCE Acinetobacter calcoaceticus.  
 ORGANISM Acinetobacter calcoaceticus  
 Eubacteria; Proteobacteria; gamma subdivision; Moraxellaceae;  
 Acinetobacter.

REFERENCE 1 (bases 1 to 2878)

Anderegg,U.

Direct Submission

Submitted (11-JUN-1992) U. Anderegg, Univ. Leipzig, Fach.

Blowissenshaften, Talstrasse 33, 0-7010 Leipzig, FRG

REFERENCE 2 (bases 1 to 2878)

Anderegg,U., Schunck,W.H., Asperger,O. and Kleber,H.P.

Unpublished

FEATURES Location/Qualifiers

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/organism="Acinetobacter calcoaceticus"

/strain="EB 104"

/db\_xref="taxon:471"

/clone="pUC 119-64"

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/db\_xref="SWISS-PROT:P31004"

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/db\_xref="PID:g38720"

/db\_xref="SWISS-PROT:P31002"

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BASE COUNT

ORIGIN

Query Match 100.0%; Score 9; DB 1; Length 2878;

Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgagtcga 9  
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 Db 2157 TCTGAGTCA 2165

RESULT 10

AE000688/c

LOCUS AE000688 14801 bp DNA BCT 30-OCT-1997

DEFINITION Aquifex aeolicus section 20 of 109 of the complete genome.

ACCESSION AE000688 AE000657

NID g2983063

KEYWORDS

SOURCE Aquifex aeolicus.

ORGANISM Aquifex aeolicus

REFERENCE 1 (bases 1 to 14801)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,

Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aulay,M.,

Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.

The complete genome of the hyperthermophilic bacterium Aquifex

aeolicus

Nature 392 (6674), 353-358 (1998)

JOURNAL

MEDLINE

REFERENCE 2 (bases 1 to 14801)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,

Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aulay,M.,

Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.

Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,

CA 92121

Direct Submission

COMMENT

Putative indicates no similarity to known proteins

Hypothetical indicates similarity to a protein of unknown function.

FEATURES Location/Qualifiers

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CDS
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/ gene="rpon"
/ gene="rpon"
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/ db_xref="PID:g2983216"
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EILKALNDLARGKKLKEIKRSLRLLPLSSAAEKYTFKADVDAIIEENGEEFFI
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BASE COUNT 4344 a 2784 c 3074 g 3948 t
ORIGIN

Query Match 100.0%; Score 9; DB 1; Length 14150;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | |
Db 2254 TCTGAGTCA 2246

RESULT 13

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BASE COUNT 4344 a 2784 c 3074 g 3948 t
ORIGIN

Query Match 100.0%; Score 9; DB 1; Length 14150;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtc 9
| | | | |
Db 2254 TCTGAGTCA 2246

RESULT 13

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AE000723 15467 bp DNA BCT 30-OCT-1997  
 LOCUS Aquifex aeolicus section 55 of 109 of the complete genome.  
 DEFINITION  
 ACCESSION AE000723 AE000657  
 NID 92983569  
 KEYWORDS  
 SOURCE Aquifex aeolicus.  
 ORGANISM Aquifex aeolicus.  
 Eubacteria; Aquificales; Aquificaceae; Aquifex.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 15467)  
 Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,  
 Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., AuJay, M.,  
 Huber, R., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V.  
 The complete genome of the hyperthermophilic bacterium Aquifex  
 aeolicus  
 JOURNAL Nature 392 (6674), 353-358 (1998)  
 MEDLINE 98196666  
 REFERENCE 2 (bases 1 to 15467)  
 AUTHORS Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,  
 Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., AuJay, M.,  
 Huber, R., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,  
 CA 92121  
 COMMENT Putative indicates no similarity to known proteins  
 Hypothetical indicates similarity to a protein of unknown function.  
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J. Bacteriol. 179 (22), 7135-7155 (1997)
98037514
REFERENCE
2 (bases 1 to 16071)
AUTHORS
Smith, D.R.
TITLE
Direct Submission
JOURNAL
Submitted (10-AUG-1997) Genomics and Technology Development, Genome
Therapeutics Corporation, 100 Beaver Street, Waltham, MA
02154-8448, USA
FEATURES
source
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/strain="delta H"
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PGVYVSGDLVSETPAVKVPYIPDPLVGLDDELEVAQLGVGREHAKWEPTTACA
YKYYPRIESEDCECEICIEACPRDVLGSESGKPVVDLENCMSCKSCVRACDKRAI
DVGVEGKFIETIDGSDVPDKDILLKADILDRKAEQVITFCEGG"
gene
9689. .10054
/genes="MTH38"
CDS
9689. .10054
/genes="MTH38"
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Ribosomal proteins; similar to, sp:LN:R18E_METJA
AC:P54022, p()-2.2E-31, pid=52%"
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RAAVNLSKINRHSDEDETIVLPKGLVGSNLDHRVQVVALSFQATRKIERAGECL
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gene
10056. .10904
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CDS      10056..10904
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AC:P54023, p()=1.4E-34, pid=25%"
/ codon_start=1
/ transl_table=11
/ product="ribosomal protein S16 (E.coli S9)"
/ db_xref="PID:g2621075"
/ translation="MLMIINGEGHILGRLASVYSKLLGEEVIVLNAEKILITGSK
EWYGYKQKDRIDRISANPRMGPKYPRPDIFRVTVMGLPKYKSKGREAKGLKA
YVGIPREFKDEIVEIDAKAGSKIKKGNELGEISELLGARLIGSVIMKXVITVYGR
KTALARTIRGKGRKVRINKVPVLEIYTPELARKIMEPLKLAGDVINDVINYVSKR
GIVGOAARNVIAIAGLVDTSDMDLKEKTVQVDRTMLVGDPRRSEPKKYGGRGAR
RQKSYR"
/ gene="MTH40"
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/ note="Function Code:10.02 - Metabolism of Macromolecules,
Transcription-mRNA synthesis and modification (includes
regulators) ; similar to, sp:LN:RPN_METJA, p()=2.20E-15,
pid=4%"
/ codon_start=1
/ transl_table=11
/ product="DNA-dependent RNA polymerase, subunit N"
/ db_xref="PID:g2621076"
/ translation="MIPVRLSCGKPKVSAYFNEVQRVADGDPKVDLDDLGLKRYCC
RRMLISHVETW"
/ gene="MTH41"
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/ gene="MTH42"
/ gene="MTH42"
/ gene="MTH42"
/ note="Function Code:10.02 - Metabolism of Macromolecules,
Transcription-mRNA synthesis and modification (includes
regulators) ; similar to, sp:LN:RPB6_CAEEL AC:Q17684,
p()=1.4E-11, pid=43%"
/ codon_start=1
/ transl_table=11
/ product="DNA-dependent RNA polymerase, subunit K"
/ db_xref="PID:g2621077"
/ translation="MHWASKLITFEARLIGARLQISMGARPIVEIKESLDPVDIA
RKEKKVMDVRRDK"
/ gene="MTH43"
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/ gene="MTH43"
/ note="Function Code:1.01 - Carbohydrate Metabolism,
Glycolysis- Gluconeogenesis ; similar to, sp:LN:ENO_HALMA
AC:P29201, p()=4.4E-95, pid=48%"
/ codon_start=1
/ transl_table=11
/ product="enolase"
/ db_xref="PID:g2621078"
/ translation="MESILEDVRVKILDSRGNPTVEVDIWNFGRAAAPSASTG
SREVAFPSCGVDEITEVEDIISSELIGMDVLDQIDLVLEKIDGTENLSLGGT
VVAVSMATAKAASNNMPLYRFLGNLATSIPIPLNNINGAHAGKNAPDIEFLV
VPVGAEDITAVFANAARVHRIRIELIKQKDPSPAGKGDEGWPVSLSGDALEIQAT
ACEVTDDELGVVEVPDLAAEFPDPEIEKYVYQENYQKDTGEGIEVEKTIETFD
MYVDEPLHGDGLGFAELTSLVGDRCMIGDDIFVTNREILREGTEMGAANAIIKP
NOIGLTDVTLTVKLALENRYTPVSHRSRSETTDDIIAHLAVAFGLPKITGAIGER
IAKINELIRQEEIPIYSRMADLPF"
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/ note="Function Code:10.04 - Metabolism of Macromolecules,

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Ribosomal proteins; similar to, sp:LN:RS2_METJA AC:P54109,
p()=2.7E-63, pid=57%"
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/ db_xref="PID:g2621079"
/ translation="MSELLIPLDKYLAAGLHIGTQOKTADMEKYIYVRSDGLVLDI
RKTNDVIAASKFLSKYBPDDILAVSTRQYGEVPKFEVGTGARTIPGRFIPGLTN
PNYAKFIEPELVATDPDSQOAIIEAKQIGIPVALCDTENLGNVDIALPVNKKGR
KAIALVYLLARQFLREKGIKLEDEDDIPPEFELKI"
/ gene="MTH45"
/ gene="MTH45"
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/ note="Function Code:14.01 - Unknown, Conserved protein;
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/ codon_start=1
/ transl_table=11
/ product="conserved protein"
/ db_xref="PID:g2621080"
/ translation="MISRPVAGAFYEDPAALRRRIEWCHEHELPGTLPVCSMR
IKGYAPAGHYSGPVNAHAYHELVSQDIPGTLVILICPNHITMGSGVSLMQQAWET
PLGTVIIDEELAEAIIVRESGILDLDETAHLAEHCEVHPVPIQYTFNFRIVPTMM
QGHETADVGHAVASAIRETGRDAVIASTDFTHYSPQIAEATDRIIDRIAMDIT
GMVYISELNATMCGYGPVAATIIASRIILGATECDLLRYATSGDVTGDRSSVGYAHL
S"
/ gene="MTH46"
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/ note="Function Code:3.01 - Lipid Metabolism, Fatty acid
biosynthesis ; similar to, sp:LN:KIME_METH AC:Q50559,
p()=6.8E-138, pid=87%"
/ codon_start=1
/ transl_table=11
/ product="mevalonate kinase"
/ db_xref="PID:g2621081"
/ translation="MKSSASAPAKAIFLGEHAVVYKPAIAAADRVTVTVSESST
HVTIPSLGIRHSSERPSPGILDYIGRCLELYHDASPLDIRVEMEIPAGSLGSSAALT
VALICPLDRYHGRDHGPGETAAARHVEVDVQGAASPLDTAISTYGLGLYLDQRRVR
QFADLGLDLVIAHLDYSGETARVAGVAERFRFPDIMGIMDTVESITITAYRELUR
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/ note="Function Code:14.01 - Unknown, Conserved protein;
similar to, sp:LN:Y044_METJA AC:Q60352, p()=3.5E-31,
pid=36%"
/ codon_start=1
/ transl_table=11
/ product="conserved protein"
/ db_xref="PID:g2621082"
/ translation="MIILKGGSVITRKDSEPAIDRNLRIEASEIGNASPSSLMTIV
HGAGFGHPFAGERYRIGISEIENEEDLRRRFGFALQNVKVLNSHVCDALLAEGIPA
VSMQPSAFIRAHAGRISHADISLIRSYLESGMPVYGVVLDSDRLKFSVIGDOL
INHPSLRMPERVILGTDVGVYTRPKPKHPDARLLDVIGSLDDELSTLDTNDVTG
GMVCKIRELLLLAEKGYESEIINAAVFNRIALLGEEVGRITRGKH"
BASE COUNT      4674 a 3602 c 4502 g 3293 t
ORIGIN

Query Match      100.0%; Score 9; DB 1; Length 16071;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 tctgagtcga 9
        |||||
Db      15645 TCTGAGTCA 15637

RESULT 15

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87% ID to interval 408704"
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83% ID to interval 8984"
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83% ID to interval 5547"
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90% ID to interval 4002"
BASE COUNT 2774 a 2581 c 2533 g 3044 t
ORIGIN

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Query Match 100.0%; Score 9; DB 1; Length 10932;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tctgagtcga 9
Db 1267 TCTGAGTCA 1259

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Search completed: June 24, 1999, 01:30:01  
Job time: 2989 sec

